

Docket No. 1110-0307P

submitted herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a disk copy of the Substitute Sequence Listing. The disk copy of the Substitute Sequence Listing, file "2002-12-06 1110-0307P.txt", is identical to the paper copy, except that it lacks formatting.

The amendment to the Specification is being made to replace the Sequence Listing as filed with the enclosed substitute Sequence Listing, which is compliant with the USPTO sequence requirements. No new matter is introduced by this amendment.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,

BIRCH, STEWART, KOLASCH & BIRCH, LLP

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GMM/MAA/CVC
1110-0307P

Attachments: Disk Copy of Sequence Listing
 Paper Copy of Sequence Listing
 Copy of Notice to Comply

(Rev. 03/27/01)

<210> 2
<211> 127
<212> PRT
<213> Mus sp.

<400> 2
Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln
1 5 10 15

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
20 25 30

Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
50 55 60

Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Ser Leu Thr Ile Ser
85 90 95

Asn Leu Glu Gln Gly Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Ser
100 105 110

Thr Leu Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
115 120 125


<210> 3
<211> 408
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(408)

<400> 3
atg gat tgg gtg tgg acc ttg cta ttc ctg ata gca gct gcc caa agt 48
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
1 5 10 15

gcc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag 96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
20 25 30

cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc 144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

aca gaa tat cca atg cac tgg gtg aag cag gct cca gga aag ggt ttc 192
Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
50 55 60

aag tgg atg ggc atg ata tac acc gac act gga gag cca tca tat gct 240
2

Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
 65 70 75 80
 gaa gag ttc aag ggg cgg ttt gcc ttc tct ttg gag acc tct gcc agc 288
 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 85 90 95
 act gcc tat ttg cag atc aac ttc ctc aaa aat gag gac acg gct aca 336
 Thr Ala Tyr Leu Gln Ile Asn Phe Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110
 tat ttc tgt gta aga ttt tac tgg gat tac ttt gac tac tgg ggc caa 384
 Tyr Phe Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
 115 120 125
 ggc acc act ctc aca gtc tcc tca 408
 Gly Thr Thr Leu Thr Val Ser Ser
 130 135

<210> 4
 <211> 136
 <212> PRT
 <213> Mus sp.

<400> 4
 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
 1 5 10 15
 Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
 50 55 60

Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
 65 70 75 80

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 85 90 95

Thr Ala Tyr Leu Gln Ile Asn Phe Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110

Tyr Phe Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
 115 120 125

Gly Thr Thr Leu Thr Val Ser Ser
 130 135

<210> 5
 <211> 381
 <212> DNA
 <213> Homo sapiens

<220>
<221> CDS
<222> (1)..(381)

<400> 5
atg gag acc gat acc ctc ctg cta tgg gtc ctc ctg cta tgg gtc cca 48
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

gga tca acc gga gat att cag atg acc cag agt ccg tcg acc ctc tct 96
Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
20 25 30

gct agc gtc ggg gat agg gtc acc ata act tgc agg gca agt cag gac 144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
35 40 45

att tcg aat tat tta aac tgg tat cag cag aag cca ggc aaa gct ccc 192
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

aag ctt cta att tat tac aca tca aga tta cac tca ggg gta cct tca 240
Lys Leu Leu Ile Tyr Tyr Ser Arg Leu His Ser Gly Val Pro Ser
65 70 75 80

cgc ttc agt ggc agt gga tct ggg acc aat tat acc ctc aca atc tcg 288
Arg Phe Ser Gly Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser
85 90 95

agt ctg cag cca gat gat ttc gcc act tat ttt tgc caa cag ggt agt 336
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Ser
100 105 110

acg ctt ccg tgg acg ttc ggt cag ggg acc aag gtg gag gtc aaa 381
Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
115 120 125

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<210> 6
<211> 127
<212> PRT
<213> Homo sapiens

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Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Ser
100 105 110

Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
115 120 125

<210> 7

<211> 408

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(408)

<400> 7

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1 5 10 15

gcc caa gca cag gtc cag ttg gtg cag tct gga gct gag gtg aag aag 96
Ala Gln Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct gga agc tca gtc aag gtg tcc tgc aaa gct tct ggg tat acc ttc 144
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

aca gaa tat cca atg cac tgg gtg aga cag gct cca gga cag ggt ttc 192
Thr Glu Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
50 55 60

aag tgg atg ggc atg ata tac acc gac act gga gag cca tca tat gct 240
Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
65 70 75 80

gaa gag ttc aag gga cgg ttt aca ttc act ttg gac acc tct acc aac 288
Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Asn
85 90 95

act gcc tat atg gag ctc agc tct ctc agg tct gag gac acg gct gtc 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tat tac tgt gta aga ttt tac tgg gat tac ttt gac tac tgg ggt caa 384
Tyr Tyr Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
115 120 125

ggt acc ctg gtc aca gtc tcc tca 408
Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 8

<211> 136

<212> PRT
<213> Homo sapiens

<400> 8
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
1 5 10 15
Ala Gln Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Glu Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
50 55 60
Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
65 70 75 80
Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Asn
85 90 95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
115 120 125
Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 9
<211> 1182
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (36)..(1169)

<400> 9
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Met Leu Gly Ile Trp Thr
1 5
ctc cta cct ctg gtt ctg act agt gtc gct act cag aac ttg gaa ggc 101
Leu Leu Pro Leu Val Leu Thr Ser Val Ala Thr Gln Asn Leu Glu Gly
10 15 20
ctg cat cat gat ggc caa ttc tgc cat aag ccc tgt cct cca ggt gaa 149
Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro Gly Glu
25 30 35
agg aaa gct agg gac tgc aca gtc aat ggg gat gaa cca gac tgc gtg 197
Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro Asp Cys Val
40 45 50
ccc tgc caa gaa ggg aag gag tac aca gac aaa gcc cat ttt tct tcc 245

Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His Phe Ser Ser
 55 60 65 70

aaa tgc aga aga tgt aga ttg tgt gat gaa gga cat ggc tta gaa gtg 293
 Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly Leu Glu Val
 75 80 85

gaa ata aac tgc acc cgg acc cag aat acc aag tgc aga tgt aaa cca 341
 Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg Cys Lys Pro
 90 95 100

aac ttt ttt tgt aac tct act gta tgt gaa cac tgt gac cct tgc acc 389
 Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp Pro Cys Thr
 105 110 115

aaa tgt gaa cat gga atc atc aag gaa tgc aca ctc acc agc aac acc 437
 Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr Ser Asn Thr
 120 125 130

aag tgc aaa gag gaa gga tcc aga tct aac gag ccc aaa tct tgt gac 485
 Lys Cys Lys Glu Gly Ser Arg Ser Asn Glu Pro Lys Ser Cys Asp
 135 140 145 150

aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga 533
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 155 160 165

ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc 581
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 170 175 180

tcc ccg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac gaa 629
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 185 190 195

B1
CONT

gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat 677
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 200 205 210

aat gcc aag aca aag ccg ccg gag gag cag tac aac agc acg tac cgt 725
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 215 220 225 230

gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag 773
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 235 240 245

gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag 821
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 250 255 260

aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac 869
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 265 270 275

acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg 917
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 280 285 290

acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg 965
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 295 300 305 310

 gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg 1013
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 315 320 325

 ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg gac 1061
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 330 335 340

 aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat 1109
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 345 350 355

 gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg 1157
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 360 365 370

 ggt aaa tga tag ggtaccccttct gag 1182
 Gly Lys
 375

<210> 10
 <211> 376
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1 5 10 15

B1
 Cmt

Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys
 20 25 30

Pro Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly
 35 40 45

Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp
 50 55 60

Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu
 65 70 75 80

Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr
 85 90 95

Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu
 100 105 110

His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys
 115 120 125

Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn
 130 135 140

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

145

150

155

160

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
165 170 175

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
180 185 190

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
195 200 205

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
210 215 220

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
225 230 235 240

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
245 250 255

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
260 265 270

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
275 280 285

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
290 295 300

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
305 310 315 320

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
325 330 335

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
340 345 350

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
355 360 365

Ser Leu Ser Leu Ser Pro Gly Lys
370 375

<210> 11

<211> 531

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36)..(518)

<400> 11

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Met Leu Gly Ile Trp Thr
1 5

ctc cta cct ctg gtt ctg act agt gtc gct act cag aac ttg gaa ggc 101
 Leu Leu Pro Leu Val Leu Thr Ser Val Ala Thr Gln Asn Leu Glu Gly
 10 15 20

ctg cat cat gat ggc caa ttc tgc cat aag ccc tgt cct cca ggt gaa 149
 Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro Gly Glu
 25 30 35

agg aaa gct agg gac tgc aca gtc aat ggg gat gaa cca gac tgc gtg 197
 Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro Asp Cys Val
 40 45 50

ccc tgc caa gaa ggg aag gag tac aca gac aaa gcc cat ttt tct tcc 245
 Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His Phe Ser Ser
 55 60 65 70

aaa tgc aga aga tgt aga ttg tgt gat gaa gga cat ggc tta gaa gtg 293
 Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly Leu Glu Val
 75 80 85

gaa ata aac tgc acc cgg acc cag aat acc aag tgc aga tgt aaa cca 341
 Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg Cys Lys Pro
 90 95 100

aac ttt ttt tgt aac tct act gta tgt gaa cac tgt gac cct tgc acc 389
 Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp Pro Cys Thr
 105 110 115

aaa tgt gaa cat gga atc atc aag gaa tgc aca ctc acc agc aac acc 437
 Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr Ser Asn Thr
 120 125 130

aag tgc aaa gag gaa gga tcc aga tct aac gag ccc aaa tct tgt gac 485
 Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Glu Pro Lys Ser Cys Asp
 135 140 145 150

aaa act cac aca tgc cca ccg tgc cca tag tga ggtacttct gag 531
 Lys Thr His Thr Cys Pro Pro Cys Pro
 155

B
 CPT
 <210> 12
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 12
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 1 5 10 15

Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys
 20 25 30

Pro Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly
 35 40 45

Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp
 50 55 60

Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu
65 70 75 80

Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr
85 90 95

Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu
100 105 110

His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys
115 120 125

Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn
130 135 140

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
145 150 155